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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Immunomedics, Inc.
- (B) STREET: 300 American Road
- (C) CITY: Morris Plains
- (D) STATE: New Jersey
- (E) COUNTRY: USA
- (F) ZIP: 07950

(ii) TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
AND FOR TARGETING APPLICATIONS

(iii) NUMBER OF SEQUENCES: 45

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(v) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT/US97/04696
- (B) FILING DATE: 19-MAR-1997

(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 60/013,708
- (B) FILING DATE: 20-MAR-1996

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Asn Tyr Trp Met Thr
1 5

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ser Ile Thr Ser Thr Gly Gly Thr Tyr His Ala Glu Ser Val Lys Gly
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asp Asp Tyr Gly Gly Gln Ser Thr Tyr Val Met Asp Ala
 1 5 10

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Arg Ala Ser Gln Asp Ile Gly Asn Tyr Leu Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gly Ala Thr Asn Leu Ala Ala
 1 5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGAGGAGACG GTGACCGTGG TCCCTTGGCC CC

32

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGATGATGTC TTATGAACAA

20

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCAGTTCCGA GCTCGTGCTC ACCCAGTCTC CA

32

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCAGTTCCGA GCTCCAGATG ACCCAGTCTC CA

32

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCAGATGTGA GCTCGTGATG ACCCAGACTC CA

32

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCAGATGTGA GCTCGTCATG ACCCAGTCTC CA

32

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCAGTTCCGA GCTCGTGATG ACACAGTCTC CA

32

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- ```
(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "primer"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTTAGATCTC CAGCTTGGTC CC

22

- (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 122 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Val | Gln | Leu | Val | Glu | Ser | Gly | Gly | Gly | Val | Val | Gln | Pro | Gly | Arg |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Leu | Arg | Leu | Ser | Cys | Ser | Ser | Ser | Gly | Phe | Ile | Phe | Ser | Xaa | Xaa |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Xaa | Xaa | Xaa | Trp | Val | Arg | Gln | Ala | Pro | Gly | Lys | Gly | Leu | Glu | Trp | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa |
|     | 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Xaa | Xaa | Arg | Phe | Thr | Ile | Ser | Arg | Asp | Asn | Ser | Lys | Asn | Thr | Leu | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | Gln | Met | Asp | Ser | Leu | Arg | Pro | Glu | Asp | Thr | Gly | Val | Tyr | Phe | Cys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Arg | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Trp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Gln | Gly | Thr | Pro | Val | Thr | Val | Ser | Ser |     |     |     |     |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |

- (2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 122 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Gln | Val | Gln | Leu | Gln | Glu | Ser | Gly | Gly | Asp | Leu | Val | Gln | Pro | Gly | Arg | 1   | 5   | 10  | 15 |
| Ser | Leu | Lys | Leu | Ser | Cys | Val | Ala | Ser | Gly | Phe | Thr | Phe | Ser | Asn | Tyr | 20  | 25  | 30  |    |
| Trp | Met | Thr | Trp | Ile | Arg | Gln | Ala | Pro | Gly | Glu | Gly | Leu | Glu | Trp | Val | 35  | 40  | 45  |    |
| Ala | Ser | Ile | Thr | Ser | Thr | Gly | Gly | Gly | Thr | Tyr | His | Ala | Glu | Ser | Val | 50  | 55  | 60  |    |
| Lys | Gly | Arg | Phe | Thr | Ile | Ser | Arg | Asp | Asn | Ser | Lys | Ser | Thr | Leu | Tyr | 65  | 70  | 75  | 80 |
| Leu | Gln | Met | Asn | Ser | Leu | Arg | Pro | Glu | Asp | Thr | Ala | Thr | Tyr | Tyr | Cys | 85  | 90  | 95  |    |
| Ser | Arg | Asp | Asp | Tyr | Gly | Gly | Gln | Ser | Thr | Tyr | Val | Met | Asp | Ala | Trp | 100 | 105 | 110 |    |
| Gly | Gln | Gly | Ser | Ser | Val | Thr | Val | Ser | Ser | 115 | 120 |     |     |     |     |     |     |     |    |

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |    |    |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|----|----|----|
| Gln | Val | Gln | Leu | Gln | Glu | Ser | Gly | Gly | Gly | Val | Val | Gln | Pro | Gly | Arg | 1  | 5  | 10 | 15 |
| Ser | Leu | Arg | Leu | Ser | Cys | Ser | Ser | Ser | Gly | Phe | Thr | Phe | Ser | Asn | Tyr | 20 | 25 | 30 |    |
| Trp | Met | Thr | Trp | Ile | Arg | Gln | Ala | Pro | Gly | Lys | Gly | Leu | Glu | Trp | Val | 35 | 40 | 45 |    |
| Ala | Ser | Ile | Thr | Ser | Thr | Gly | Gly | Gly | Thr | Tyr | His | Ala | Glu | Ser | Val | 50 | 55 | 60 |    |
| Lys | Gly | Arg | Phe | Thr | Ile | Ser | Arg | Asp | Asn | Ser | Lys | Asn | Thr | Leu | Phe | 65 | 70 | 75 | 80 |



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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Figure 1 consists of two scatter plots. The left plot shows a positive correlation between the number of children and the number of mothers, with a regression line indicating a positive slope. The right plot shows a negative correlation between the number of children and the number of mothers, with a regression line indicating a negative slope.

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1 5 10 15  
 Asp Arg Val Thr Ile Thr Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 20 25 30  
 Xaa Xaa Trp Tyr Gln Gln Thr Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45  
 Tyr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80  
 Glu Asp Ile Ala Thr Tyr Tyr Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 85 90 95  
 Xaa Phe Gly Gln Gly Thr Lys Leu Gln Ile Thr Arg Thr  
 100 105

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Pro Ala Ser Leu Gly  
 1 5 10 15  
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Gly Asn Tyr  
 20 25 30  
 Leu Arg Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Arg Leu Leu Ile  
 35 40 45  
 Tyr Gly Ala Thr Asn Leu Ala Ala Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60  
 Ser Arg Ser Gly Ser Asp Phe Ser Leu Thr Ile Asn Ser Leu Glu Ser  
 65 70 75 80  
 Glu Asp Met Ala Ile Tyr Tyr Cys Leu His His Ser Glu Tyr Pro Tyr  
 85 90 95  
 Thr Phe Gly Ile Gly Thr Lys Leu Glu Arg Lys Arg  
 100 105

## (2) INFORMATION FOR SEQ ID NO:23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Gly Asn Tyr
 20 25 30
Leu Arg Trp Phe Gln Gln Thr Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
Tyr Gly Ala Thr Asn Leu Ala Ala Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
Ser Arg Ser Gly Ser Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
Glu Asp Ile Ala Thr Tyr Tyr Cys Leu His His Ser Glu Tyr Pro Tyr
 85 90 95
Thr Phe Gly Ile Gly Thr Lys Leu Gln Ile Lys Arg
 100 105

```

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Gly Asn Tyr
 20 25 30
Leu Arg Trp Phe Gln Gln Thr Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
Tyr Gly Ala Thr Asn Leu Ala Ala Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

```

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80  
 Glu Asp Ile Ala Thr Tyr Tyr Cys Leu His His Ser Glu Tyr Pro Tyr  
 85 90 95  
 Thr Phe Gly Ile Gly Thr Lys Leu Gln Ile Lys Arg  
 100 105

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..366

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CAG GTC CAA CTG CAG GAG TCA GGG GGA GGT GTA GTG CAG CCT GGA AGG | 48  |
| Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg |     |
| 1 5 10 15                                                       |     |
| TCT CTG AGA CTT TCC TGT AGC TCA TCT GGA TTC ACA TTC AGT AAT TAC | 96  |
| Ser Leu Arg Leu Ser Cys Ser Ser Ser Gly Phe Thr Phe Ser Asn Tyr |     |
| 20 25 30                                                        |     |
| TGG ATG ACT TGG ATA CGC CAG GCT CCA GGG AAG GGT CTT GAA TGG GTT | 144 |
| Trp Met Thr Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val |     |
| 35 40 45                                                        |     |
| GCG TCC ATT ACT AGT ACT GGT GGT GGT ACC TAC CAT GCA GAG TCT GTG | 192 |
| Ala Ser Ile Thr Ser Thr Gly Gly Gly Thr Tyr His Ala Glu Ser Val |     |
| 50 55 60                                                        |     |
| AAG GGC CGA TTC ACT ATC TCC AGA GAT AAT TCA AAA AAC ACC CTG TTC | 240 |
| Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe |     |
| 65 70 75 80                                                     |     |
| CTG CAA ATG GAC AGT CTG AGG CCT GAG GAC ACG GGC GTT TAT TAC TGT | 288 |
| Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Tyr Cys |     |
| 85 90 95                                                        |     |
| TCA AGA GAT GAC TAC GGA GGA CAG AGC ACC TAT GTT ATG GAT GCC TGG | 336 |
| Ser Arg Asp Asp Tyr Gly Gly Gln Ser Thr Tyr Val Met Asp Ala Trp |     |
| 100 105 110                                                     |     |
| GGT CAG GGA ACT CCG GTC ACC GTC TCC TCC                         | 366 |
| Gly Gln Gly Thr Pro Val Thr Val Ser Ser                         |     |
| 115 120                                                         |     |

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
Ser Leu Arg Leu Ser Cys Ser Ser Ser Gly Phe Thr Phe Ser Asn Tyr
 20 25 30
Trp Met Thr Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
Ala Ser Ile Thr Ser Thr Gly Gly Gly Thr Tyr His Ala Glu Ser Val
 50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
 65 70 75 80
Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Tyr Cys
 85 90 95
Ser Arg Asp Asp Tyr Gly Gly Gln Ser Thr Tyr Val Met Asp Ala Trp
 100 105 110
Gly Gln Gly Thr Pro Val Thr Val Ser Ser
 115 120

```

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..324

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```

GAC ATT CAG ATG ACC CAG TCT CCA TCT TCC CTG TCT GCG TCT GTG GGA 48
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

GAC AGA GTC ACT ATT ACT TGC CGG GCA AGT CAA GAC ATT GGA AAT TAT 96
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Gly Asn Tyr
 20 25 30

```

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| TTA AGA TGG TTC CAG CAG ACA CCG GGG AAA GCT CCG AAA CTT TTG ATT | 144 |
| Leu Arg Trp Phe Gln Gln Thr Pro Gly Lys Ala Pro Lys Leu Leu Ile |     |
| 35 40 45                                                        |     |
| TAT GGT GCA ACC AAC TTG GCT GCA GGG GTC CCA TCA CGG TTC AGT GGC | 192 |
| Tyr Gly Ala Thr Asn Leu Ala Ala Gly Val Pro Ser Arg Phe Ser Gly |     |
| 50 55 60                                                        |     |
| AGT GGG TCT GGG ACA GAT TTT ACT TTT ACC ATC TCA AGC CTT CAG CCT | 240 |
| Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro |     |
| 65 70 75 80                                                     |     |
| GAA GAT ATT GCT ACT TAT TAC TGT CTG CAC CAT TCT GAG TAT CCA TAC | 288 |
| Glu Asp Ile Ala Thr Tyr Tyr Cys Leu His His Ser Glu Tyr Pro Tyr |     |
| 85 90 95                                                        |     |
| ACG TTT GGA ATT GGG ACC AAG TTG CAG ATC AAA CGT G               | 325 |
| Thr Phe Gly Ile Gly Thr Lys Leu Gln Ile Lys Arg                 |     |
| 100 105                                                         |     |

## (2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 108 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly |  |
| 1 5 10 15                                                       |  |
| Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Gly Asn Tyr |  |
| 20 25 30                                                        |  |
| Leu Arg Trp Phe Gln Gln Thr Pro Gly Lys Ala Pro Lys Leu Leu Ile |  |
| 35 40 45                                                        |  |
| Tyr Gly Ala Thr Asn Leu Ala Ala Gly Val Pro Ser Arg Phe Ser Gly |  |
| 50 55 60                                                        |  |
| Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro |  |
| 65 70 75 80                                                     |  |
| Glu Asp Ile Ala Thr Tyr Tyr Cys Leu His His Ser Glu Tyr Pro Tyr |  |
| 85 90 95                                                        |  |
| Thr Phe Gly Ile Gly Thr Lys Leu Gln Ile Lys Arg                 |  |
| 100 105                                                         |  |

## (2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 324 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| GAC ATT CAG CTG ACC CAG TCT CCA GCT TCC CTG CCT GCG TCT CTG GGA | 48  |
| Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Pro Ala Ser Leu Gly |     |
| 1 5 10 15                                                       |     |
| GAC AGA GTC ACT ATT ACT TGC CGG GCA AGT CAA GAC ATT GGA AAT TAT | 96  |
| Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Gly Asn Tyr |     |
| 20 25 30                                                        |     |
| TTA AGA TGG TTC CAG CAG AAA CCG GGG AAA TCT CCG AGG CTT TTG ATT | 144 |
| Leu Arg Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Arg Leu Leu Ile |     |
| 35 40 45                                                        |     |
| TAT GGT GCA ACC AAC TTG GCA GCT GGG GTC CCA TCA CGG TTC AGT CGC | 192 |
| Tyr Gly Ala Thr Asn Leu Ala Ala Gly Val Pro Ser Arg Phe Ser Arg |     |
| 50 55 60                                                        |     |
| AGT AGG TCT GGG TCA GAT TTT TCT CTG ACC ATC AAC AGC CTG GAG TCT | 240 |
| Ser Arg Ser Gly Ser Asp Phe Ser Leu Thr Ile Asn Ser Leu Glu Ser |     |
| 65 70 75 80                                                     |     |
| GAA GAT ATG GCT ATT TAT TAC TGT CTG CAC CAT TCT GAG TAT CCA TAC | 288 |
| Glu Asp Met Ala Ile Tyr Tyr Cys Leu His His Ser Glu Tyr Pro Tyr |     |
| 85 90 95                                                        |     |
| ACG TTT GGA ATT GGG ACC AAG CTG GAA CGG AAA CGG                 | 324 |
| Thr Phe Gly Ile Gly Thr Lys Leu Glu Arg Lys Arg                 |     |
| 100 105                                                         |     |

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

|                                                                 |
|-----------------------------------------------------------------|
| Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Pro Ala Ser Leu Gly |
| 1 5 10 15                                                       |
| Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Gly Asn Tyr |
| 20 25 30                                                        |
| Leu Arg Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Arg Leu Leu Ile |
| 35 40 45                                                        |
| Tyr Gly Ala Thr Asn Leu Ala Ala Gly Val Pro Ser Arg Phe Ser Arg |
| 50 55 60                                                        |

Ser Arg Ser Gly Ser Asp Phe Ser Leu Thr Ile Asn Ser Leu Glu Ser  
65 70 75 80

Glu Asp Met Ala Ile Tyr Tyr Cys Leu His His Ser Glu Tyr Pro Tyr  
85 90 95

Thr Phe Gly Ile Gly Thr Lys Leu Glu Arg Lys Arg  
100 105

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CAG GTC CAA CTG CAG GAG TCA GGG GGA GAT CTA GTG CAG CCT GGA AGG | 48  |
| Gln Val Gln Leu Gln Glu Ser Gly Gly Asp Leu Val Gln Pro Gly Arg |     |
| 1 5 10 15                                                       |     |
| TCT CTG AAA CTT TCC TGT GTA GCC TCT GGA TTC ACA TTC AGT AAT TAC | 96  |
| Ser Leu Lys Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Asn Tyr |     |
| 20 25 30                                                        |     |
| TGG ATG ACT TGG ATC CGC CAG GCT CCA GGG GAG GGT CTT GAA TGG GTT | 144 |
| Trp Met Thr Trp Ile Arg Gln Ala Pro Gly Glu Gly Leu Glu Trp Val |     |
| 35 40 45                                                        |     |
| GCG TCC ATT ACT AGT ACT GGT GGT GGG ACT TAC CAT GCA GAG TCT GTG | 192 |
| Ala Ser Ile Thr Ser Thr Gly Gly Gly Thr Tyr His Ala Glu Ser Val |     |
| 50 55 60                                                        |     |
| AAG GGC CGA TTC ACT ATC TCC AGA GAT AAT TCA AAA AGC ACC CTG TAC | 240 |
| Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Ser Thr Leu Tyr |     |
| 65 70 75 80                                                     |     |
| CTG CAA ATG AAC AGT CTG AGG CCT GAG GAC ACG GCC ACT TAT TAC TGT | 288 |
| Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Thr Tyr Tyr Cys |     |
| 85 90 95                                                        |     |
| TCA AGA GAT GAC TAC GGA GGA CAG AGC ACC TAT GTT ATG GAT GCC TGG | 336 |
| Ser Arg Asp Asp Tyr Gly Gly Gln Ser Thr Tyr Val Met Asp Ala Trp |     |
| 100 105 110                                                     |     |
| GGT CAG GGA TCT TCG GTC ACC GTC TCC TCA                         | 366 |
| Gly Gln Gly Ser Ser Val Thr Val Ser Ser                         |     |
| 115 120                                                         |     |



## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

Gln Val Gln Leu Gln Glu Ser Gly Gly Asp Leu Val Gln Pro Gly Arg
 1 5 10 15
Ser Leu Lys Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Asn Tyr
 20 25 30
Trp Met Thr Trp Ile Arg Gln Ala Pro Gly Glu Gly Leu Glu Trp Val
 35 40 45
Ala Ser Ile Thr Ser Thr Gly Gly Gly Thr Tyr His Ala Glu Ser Val
 50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Ser Thr Leu Tyr
 65 70 75 80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95
Ser Arg Asp Asp Tyr Gly Gly Gln Ser Thr Tyr Val Met Asp Ala Trp
 100 105 110
Gly Gln Gly Ser Ser Val Thr Val Ser Ser
 115 120

```

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligo"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CAGGTCCAAC TGCAGGAGTC AGGGGGAGGT GTAGTGCAGC CTGGAA

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligo"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AGTAATGGAC GCAACCCATT CAAGACCCTT CCCTGGAGCC TGGCGTATCC AAGTCATCCA | 60  |
| GTAATTACTG AATGTGAATC CAGATGAGCT ACAGGAAAGT CTCAGAGACC TTCCAGGCTG | 120 |
| CACTACACCT                                                        | 130 |

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 48 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligo"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

|                                                       |    |
|-------------------------------------------------------|----|
| ATGCAGAGTC TGTGAAGGGC CGATTCACCTA TCTCCAGAGA TAATTCAA | 48 |
|-------------------------------------------------------|----|

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 54 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligo"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

|                                                             |    |
|-------------------------------------------------------------|----|
| TTCACAGACT CTGCATGGTA GGTACCACCA CCAGTACTAG TAATGGACGC AACC | 54 |
|-------------------------------------------------------------|----|

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 133 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligo"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ACCCCAGGCA TCCATAACAT AGGTGCTCTG TCCTCCGTAG TCATCTCTTG AACAGTAATA 60  
 AACGCCCCTG TCCTCAGGCC TCAGACTGTC CATTGTCAGG AACAGGGTGT TTTTGAATT 120  
 ATCTCTGGAG ATA 133

## (2) INFORMATION FOR SEQ ID NO:38:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligo"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GGAGGAGACG GTGACCGGAG TTCCCTGACC CCAGGCATCC ATAAC 45

## (2) INFORMATION FOR SEQ ID NO:39:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligo"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GACATTCAGC TGACCCAGTC TCCATCTTCC CTGTCTGCGT CTGTGGGAGA 50

## (2) INFORMATION FOR SEQ ID NO:40:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligo"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATGACCCAGT CTCCATCTTC CCTGTCTGCG TCTGTGGGAG A

41

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligo"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

AGTTGGTTGC ACCATAAATC AAAAGTTTCG GAGCTTTCCC CGGTGTCTGC TGGAACCATC 60

TTAAATAATT TCCAATGTCT TGAAGTGGCC GGCAAGTAAT AGTGACTCTG TCTCCACAG 120

ACGCAGACA 129

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligo"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TGGCTGCAGG GGTCCCATCA CGGTTTCTAGT GCAGTGGGTC TGGG 44

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligo"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GGACCCCTGC AGCCAAGTTG GTTGCACCAT AAATCA

36

## (2) INFORMATION FOR SEQ ID NO:44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligo"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```

TTGGTCCCAA TTCAAACGT GTATGGATAC TCAGATGGT GCAGACAGTA ATAAGTAGCA 60
ATATCTTCAG GCTGAAGGCT TGAGATGGTA AAAGTAAAAT CTGTCCCAGA CCCACTGCCA 120
CTGAACCG 128

```

## (2) INFORMATION FOR SEQ ID NO:45:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligo"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```

CACGTTAGAT CTGCAACTTG GTCCCAATTC CAAACGTGT 39

```